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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/061,690

DATE: 03/12/2002

TIME: 09:52:48

Input Set : N:\Cr3\RULE60\10061690.raw

Output Set: N:\CRF3\03122002\J061690.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Lal, Preeti

6 Hillman, Jennifer L.

7 Goli, Surya K.

9 (ii) TITLE OF INVENTION: NOVEL PROLINE-RICH ACIDIC PROTEIN

11 (iii) NUMBER OF SEQUENCES: 3

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.

15 (B) STREET: 3174 Porter Drive

16 (C) CITY: Palo Alto

17 (D) STATE: CA

18 (E) COUNTRY: US

19 (F) ZIP: 94304

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Diskette

23 (B) COMPUTER: IBM Compatible

24 (C) OPERATING SYSTEM: DOS

25 (D) SOFTWARE: FastSEQ Version 2.0

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/10/061,690

C--> 29 (B) FILING DATE: 01-Feb-2002

30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 09/213,396

34 (B) FILING DATE:

36 (viii) ATTORNEY/AGENT INFORMATION:

37 (A) NAME: Billings, Lucy J.

38 (B) REGISTRATION NUMBER: 36,749

39 (C) REFERENCE/DOCKET NUMBER: PF-0225 US

41 (ix) TELECOMMUNICATION INFORMATION:

42 (A) TELEPHONE: 415-855-0555

43 (B) TELEFAX: 415-845-4166

45 (2) INFORMATION FOR SEQ ID NO: 1:

47 (i) SEQUENCE CHARACTERISTICS:

48 (A) LENGTH: 151 amino acids

49 (B) TYPE: amino acid

50 (C) STRANDEDNESS: single

51 (D) TOPOLOGY: linear

53 (vii) IMMEDIATE SOURCE:

54 (A) LIBRARY: PANCTUT02

55 (B) CLONE: 2235738

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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59 Met Arg Arg Leu Leu Leu Val Thr Ser Leu Val Val Val Leu Leu Trp
60 1 5 10 15
61 Glu Ala Gly Ala Val Pro Ala Pro Lys Val Pro Ile Lys Met Gln Val
62 20 25 30
63 Lys His Trp Pro Ser Glu Gln Asp Pro Glu Lys Ala Trp Gly Ala Arg
64 35 40 45
65 Val Val Glu Pro Pro Glu Lys Asp Asp Gln Leu Val Val Leu Phe Pro
66 50 55 60
67 Val Gln Lys Pro Lys Leu Leu Thr Thr Glu Glu Lys Pro Arg Gly Gln
68 65 70 75 80
69 Gly Arg Gly Pro Ile Leu Pro Gly Thr Lys Ala Trp Met Glu Thr Glu
70 85 90 95
71 Asp Thr Leu Gly Arg Val Leu Ser Pro Glu Pro Asp His Asp Ser Leu
72 100 105 110
W--> 73 Tyr His Pro Pro Xaa Glu Glu Asp Gln Gly Glu Glu Arg Pro Arg Leu
74 115 120 125
75 Trp Val Met Pro Asn His Gln Val Leu Leu Gly Pro Glu Glu Asp Gln
76 130 135 140
W--> 77 Asp His Xaa Tyr Gln Pro Gln
78 145 150
80 (2) INFORMATION FOR SEQ ID NO: 2:
82 (i) SEQUENCE CHARACTERISTICS:
83 (A) LENGTH: 596 base pairs
84 (B) TYPE: nucleic acid
85 (C) STRANDEDNESS: single
86 (D) TOPOLOGY: linear
88 (vii) IMMEDIATE SOURCE:
89 (A) LIBRARY: PANCTUT02
90 (B) CLONE: 2235738
92 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
94 AGCCACTGCA GCTCCCTGAG CACTCTCTAC AGAGACGCGG ACCCCAGACA TGAGGAGGCT 60
95 CCTCCTGGTC ACCAGCCTGG TGGTTGTGCT GCTGTGGGAG GCAGGTGCAG TCCCAGCACC 120
96 CAAGGTCCCT ATCAAGATGC AAGTCAAACA CTGGCCCTCA GAGCAGGACC CAGAGAAGGC 180
97 CTGGGGCGCC CGTGTGGTGG AGCCTCCGGA GAAGGACGAC CAGCTGGTGG TGCTGTTCCT 240
98 TGTCCAGAAG CCGAAACTCT TGACCACCGA GGAGAAGCCA CGAGGTCAGG GCAGGGGCCC 300
99 CATCCTTCCA GGCACCAAGG CCTGGATGGA GACCGAGGAC ACCCTGGGCC GTGTCTTGAG 360
100 TCCCAGAGCC GACCATGACA GCCTGTACCA CCCTCCGNCT GAGGAGGACC AGGGCGAGGA 420
101 GAGGCCCCCG TTGTGGGTGA TGCCAAATCA CCAGGTGCTC CTGGGACCGG AGGAAGACCA 480
102 AGACCACATN TACCAACCCC AGTAGGGNTT CAGGGGCCAT NAGTGNCCCC GGCCTGTTC 540
103 AAGGCCCAGG TGTNGGATT GGACCTTCCT AACCTGCCCA GTTAGACAAA TAAAC 596
105 (2) INFORMATION FOR SEQ ID NO: 3:
107 (i) SEQUENCE CHARACTERISTICS:
108 (A) LENGTH: 149 amino acids
109 (B) TYPE: amino acid
110 (C) STRANDEDNESS: single
111 (D) TOPOLOGY: linear
113 (vii) IMMEDIATE SOURCE:
114 (A) LIBRARY: GenBank
115 (B) CLONE: 899433

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117      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
119 Met Lys Arg Phe Leu Leu Ala Thr Cys Leu Val Ala Ala Leu Leu Trp
120   1           5           10           15
121 Glu Ala Gly Ala Arg Pro Ala His Gln Val Pro Val Lys Thr Lys Gly
122           20           25           30
123 Lys His Val Phe Pro Glu Gln Glu Thr Glu Lys Val Trp Asp Thr Arg
124           35           40           45
125 Ala Leu Glu Pro Leu Glu Lys Asp Asn Gln Leu Gly Pro Leu Leu Pro
126   50           55           60
127 Glu Pro Lys Gln Lys Pro Ala Ala Ala Glu Glu Lys Arg Pro Asp Ala
128  65           70           75           80
129 Met Thr Trp Val Glu Thr Glu Asp Ile Leu Ser His Leu Arg Ser Pro
130           85           90           95
131 Leu Gln Gly Pro Glu Leu Asp Leu Asp Ser Ile Asp His Pro Met Ser
132           100          105          110
133 Asp Asp Val Gln Asp Glu Glu Val Pro Gln Ser Arg Pro Ile Leu Tyr
134           115          120          125
135 Arg Gln Val Leu Gln Gly Pro Glu Glu Asp Leu Asp His Leu Ala His
136           130          135          140
137 Ser Met Glu Asp Ser
138 145

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VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:73 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:77 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1